

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:31:49 ; Search time 20.26 Seconds
(without alignments)
430.005 Million cell updates/sec

Title: US-09-502-984B-1
Perfect score: 1194
Sequence: 1 APPPNLPDPFESKALLAA.....GGFMSAMSEPVSLTSPDLD 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1194	100.0	508	1	EPOR_HUMAN
2	982.5	82.3	507	2	EPOR_MOUSE
3	981.5	82.2	507	1	EPOR_RAT
4	205	17.2	625	1	TPOR_MOUSE
5	185	15.5	635	1	TPOR_MOUSE
6	159	13.3	581	1	PRLR_BOVIN
7	151	12.6	581	1	PRLR_BOVIN
8	148	12.4	616	1	PRLR_CERL
9	144.5	12.1	831	1	PRLR_RABIT
10	136.5	11.4	830	1	PRLR_CHICK
11	135	11.3	831	1	PRLR_COLLI
12	128	10.7	622	1	PRLR_MELGA
13	126	10.6	522	1	PRLR_HUMAN
14	126	10.6	608	1	PRLR_HUMAN
15	123.5	10.3	650	1	PRLR_MOUSE
16	122.5	10.3	634	1	GHR_MOUSE
17	121.5	10.2	634	1	GHR_BOVIN
18	121	10.1	634	1	GHR_SHEEP
19	117.5	9.8	610	1	PRLR_RAT
20	117.5	9.8	610	1	PRLR_COLLI
21	117	9.8	638	1	GHR_PIG
22	116.5	9.8	608	1	GHR_CHICK
23	116	9.7	638	1	GHR_RABIT
24	113	9.5	630	1	GHR_HUMAN
25	111.5	9.3	630	1	PRLR_CORENI
26	108.5	9.1	638	1	LIFR_HUMAN
27	107	9.0	638	1	GHR_RAT
28	107	9.0	468	1	EP2A2_HUMAN
29	106.5	8.9	378	1	IL3R_MOUSE
30	104.5	8.8	1165	1	IL3R_HUMAN
31	104	8.7	2594	1	7LES_DROVI
32	102	8.5	896	1	CYRB_MOUSE
33	101	8.5	977	1	EP2A2_MOUSE

34	100.5	8.4	917	1	IL6B_MOUSE
35	97.5	8.2	638	1	GHR_YACMU
36	97.5	8.2	1092	1	LIFR_MOUSE
37	96	8.0	1134	1	TIE1_MOUSE
38	95.5	8.0	2554	1	7LES_DROME
39	95	8.0	184	1	MPL_MPLV
40	95	8.0	993	1	EP2A2_MOUSE
41	95	8.0	1055	1	EP2A2_HUMAN
42	94.5	7.9	551	1	IL2B_HUMAN
43	92.5	7.7	459	1	IL7R_MOUSE
44	92	7.7	369	1	CYRG_HUMAN
45	92	7.7	878	1	IL3B_MOUSE

ALIGNMENTS

RESULT ID	1	EPOR_HUMAN	STANDARD:	PRT:	508 AA.
AC	P19235:	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Erythropoietin receptor precursor (EPO-R).				
GN	EPOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91372359; PubMed=1654273;				
RA	Ehrenman K., St John T.;				
RT	"The erythropoietin receptor gene: cloning and identification of				
RT	multiple transcripts in an erythroid cell line OCI-M1.";				
RT	Exp. Hematol. 19:973-977(1991).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90304340; PubMed=2163696;				
RT	Jones S.S., D'Andrea A., Haines L.L., Wong G.G.;				
RT	"Human erythropoietin receptor: cloning, expression, and biologic				
RT	characterization.";				
RL	Blood 76:31-35(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RC	MEDLINE=92399733; PubMed=1668606;				
RA	Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,				
RA	Hankins W.D.;				
RT	"Cloning of the human erythropoietin receptor gene.";				
RL	Blood 78:2548-2556(1991).				
RN	[4]				
RP	SEQUENCE OF 1-96 FROM N.A.				
RC	TISSUE=Placenta;				
RC	MEDLINE=92399734; PubMed=1668607;				
RA	Maouche L., Touramille C., Hattab C., Boffa G., Cartton J.P.,				
RA	Chretien S.;				
RT	"Cloning of the gene encoding the human erythropoietin receptor.";				
RL	Blood 78:2557-2563(1991).				
RN	[5]				
RP	SEQUENCE OF 1-17 FROM N.A.				
RC	MEDLINE=92147143; PubMed=1664413;				
RA	Penny L.A., Forget B.G.;				
RT	"Genomic organization of the human erythropoietin receptor gene.";				
RL	Genomics 11:974-980(1991).				
RN	[6]				
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.				
RC	MEDLINE=96291992; PubMed=8662530;				
RA	Livahan O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,				
RA	Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.;				
RT	"Functional mimicry of a protein hormone by a peptide agonist: the				
RT	EPO receptor complex at 2.8 A.";				

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RL Science 273:464-471(1996).
RN
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.
RX MEDLINE-99023198; PubMed-9808045;
RA Livnah O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,
RA You Y., Liu K.D., Goldsmith M.A., He W., Krause C.D., Pestka S.,
RA Jolliffe L.K., Wilson I.A.;
RT "An antagonist peptide-EPO receptor complex suggests that receptor
RT dimerization is not sufficient for activation."
RL Nat. Struct. Biol. 5:993-1004(1998).
RN
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-244 IN COMPLEX WITH EPO.
RX MEDLINE-98445092; PubMed-9774108;
RA Syed R.S., Reid S.W., Li C., Chetani J.C., Aoki K.H., Liu B.,
RA Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
RA Elliott S., Silney K., Katz B.A., Matthews D.J., Mendoloski J.J.,
RA Egrie J., Stroud R.M.;
RT "Efficiency of signalling through cytokine receptors depends
RT critically on receptor orientation."
RL Nature 395:511-516(1998).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC
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CC
DR EMBL: M34986; AAA52401.1; -
DR EMBL: M60459; AAA52403.1; -
DR EMBL: S45332; AAB3271.1; -
DR EMBL: M76595; AAA52393.1; -
DR EMBL: M77244; AAA52392.1; -
DR PIR: A43799; A43799.
DR PIR: A49824; A49824.
DR PIR: A53958; A53958.
DR PDB: 1EBP; 29-JUL-97.
DR PDB: 1EBA; 18-NOV-98.
DR PDB: 1EBR; 01-OCT-99.
DR PDB: 1CN4; 11-AUG-99.
DR MIM: 133171; -
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 508
FT DOMAIN 25 508 ERYTHROPOIETIN RECEPTOR.
FT TRASNMEM 251 273 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 274 508 POTENTIAL.
FT DOMAIN 148 213 CYTOPLASMIC (POTENTIAL).
FT DISULFID 52 62 FIBRONECTIN TYPE-III.
FT DISULFID 91 107
FT CARBOHYD 76 76
FT SEQUENCE 508 AA; 55065 MW; F9F326E162E9512A CRC64;

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Query Match 100.0%; Score 1194; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 7.3e-105;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 APPNPDPKFEKAKLLAARGPDELCTFEREDLVCFWEERAAAGVGNSTFSTOLE 60
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DB 25 APPNPDPKFEKAKLLAARGPDELCTFEREDLVCFWEERAAAGVGNSTFSTOLE 84
QY 61 DEEWKLCRLHQAPTARGAVFMCSPFTADTSFVPLELRYTAAGAPRRYHRIHINEVYL 120
DB 85 DEEWKLCRLHQAPTARGAVFMCSPFTADTSFVPLELRYTAAGAPRRYHRIHINEVYL 144
QY 121 LDAPVGLVARLADSGHVYLRMLPPETPMTSHIREVVSNGNGSVORVETLEGRTTE 180
DB 145 LDAPVGLVARLADSGHVYLRMLPPETPMTSHIREVVSNGNGSVORVETLEGRTTE 204
QY 181 CVLSNLRGRTRYFAVARARMAEPSPFGFMSAMSEPVSLTPSDLD 225
DB 205 CVLSNLRGRTRYFAVARARMAEPSPFGFMSAMSEPVSLTPSDLD 249
RESULT 2
EPOR_MOUSE STANDARD: PRT: 507 AA.
AC P14753; Q63852;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin receptor precursor (Epo-R).
GN EPOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89195238; PubMed-2539263;
RA D'Andrea A.D., Lodish H.F., Wong G.G.;
RT "Expression cloning of the murine erythropoietin receptor."
RL Cell 57:277-285(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE-91080149; PubMed-2175360;
RA Kuramochi S., Ikawa Y., Todokoro K.;
RT "Characterization of murine erythropoietin receptor genes."
RL J. Mol. Biol. 216:567-575(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-92017832; PubMed-1656233;
RA Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;
RT "Upregulated expression of the erythropoietin receptor gene caused by
RT insertion of spleen focus-forming virus long terminal repeat in a
RT murine erythroleukemia cell line."
RL Mol. Cell. Biol. 11:5527-5533(1991).
RN [4]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE-90287158; PubMed-2162479;
RA Yousoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;
RT "Structure and transcription of the mouse erythropoietin receptor
RT gene."
RL Mol. Cell. Biol. 10:3675-3682(1990).
RN [5]
RP SEQUENCE OF 1-24 FROM N.A.
RX MEDLINE-91201346; PubMed-1849897;
RA Lacombe C., Chetani S., Lemarchandel V., Mayeux P., Romeo P.H.,
RA Gisselbrecht S., Carton J.P.;
RT "Spleen focus-forming virus long terminal repeat insertional
RT activation of the murine erythropoietin receptor gene in the T3c1-2
RT friend leukemia cell line."
RL J. Biol. Chem. 266:6952-6956(1991).
RN [6]
RP NOTAGENESIS.
RX MEDLINE-93180826; PubMed-8392775;
RA Miura O., Cleveland J.L., Ihle J.N.;
RT "Inactivation of erythropoietin receptor function by point mutations
RT in a region having homology with other cytokine receptors."
RL Mol. Cell. Biol. 13:1788-1795(1993).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE

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CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: J04843; AAA37571.1; -
DR EMBL: X53081; CAA37248.1; -
DR EMBL: M38133; AAA37572.1; -
DR EMBL: M62360; AAA37582.1; -
DR EMBL: S59388; AAB20029.2; -
DR PIR: A32385; A32385.
DR PIR: A41686; A41686.
DR PIR: S13249; S13249.
DR PIR: S14081; S14081.
DR HSSP: P19235; 1EBA.
DR MGD: MGI:95408; Epor.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR SMART: PF00041; fn3; 1.
DR SMART: SM00060; fn3; 1.
DR PROSITE: PS01352; Hematopo_receptor_L_F1.
DR Receptor: Transmembrane; Glycoprotein; Signal.
FT CHAIN 1 24
FT DOMAIN 25 507 ERYTHROPOIETIN RECEPTOR.
FT TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 147 212 FIBRONECTIN TYPE-III.
FT DISULFD 52 62 BY SIMILARITY.
FT DISULFD 90 106 BY SIMILARITY.
FT CARBOHD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLCT 291 291 E -> D (IN REF. 3; AAB20029).
SQ SEQUENCE 507 AA; 55194 MW; 067657A2E26451CA CRC64;

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Query Match 82.3%; Score 982.5; DB 1; Length 507;
Best Local Similarity 83.1%; Pred. No. 5.9e-85;
Matches 187; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

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QY 1 APPPLPDPKFEKSKAALLAARGPEELCTERLEDELVCFWMEAAAGVPGNYFSYOLE 60
DB 25 ASPSPLPDPKFEKSKAALLASRGSEELCTORLEDELVCFWMEAAASGM-DFNYFSYOLE 83
QY 61 DEPWKLCRLHQAPRTAGAVFWCSLPTADTSSFVPLELKVTAASGAPRYHRYIHNEVYL 120
DB 84 GESRKSRLHQAPRTAGAVFWCSLPTADTSSFVPLELKVTAASGAPRYHRYIHNEVYL 143
QY 121 LDAPVGLVARLADESGHVVLRWLPPEETPMTHIREVDVDSAGNAGSVQRYEILLEGRT 180
DB 144 LDAPVGLVARLADESGHVVLRWLPPEETPMTHIREVDVDSAGNAGSVQRYEILLEGRT 203
QY 181 CVLSNLRGRTYRTFAVRARMAEPSPFGFWSANSEPVSLITPSDLD 225
DB 204 CVLSNLRGRTYRTFAVRARMAEPSPFGFWSANSEPVSLITPSDLD 248

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RESULT 3
EPOR_RAT STANDARD: PRT: 507 AA.
AC 007303.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)

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DE Erythropoietin receptor precursor (EPO-R).
GN EPOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93266574; PubMed=7684373;
RA Masuda S., Nagao M., Takahata K., Konishi Y., Gallyas F.,
RA Tabira T., Sasaki R.;
RT "Functional erythropoietin receptor of the cells with neural
RT characteristics. Comparison with receptor properties of erythroid
RT cells.";
RL J. Biol. Chem. 268:11208-11216(1993).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D13566; BAA02761.1; -
DR PIR: A46713; A46713.
DR HSSP: P19235; 1EBA.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; fn3; 1.
DR PROSITE: PS01352; Hematopo_receptor_L_F1.
DR Receptor: Transmembrane; Glycoprotein; Signal.
FT CHAIN 1 24
FT DOMAIN 25 507 ERYTHROPOIETIN RECEPTOR.
FT TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 147 212 FIBRONECTIN TYPE-III.
FT DISULFD 52 62 BY SIMILARITY.
FT DISULFD 90 106 BY SIMILARITY.
FT CARBOHD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 507 AA; 55499 MW; AC79AF22D06A7312 CRC64;

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Query Match 82.2%; Score 981.5; DB 1; Length 507;
Best Local Similarity 82.7%; Pred. No. 7.4e-85;
Matches 186; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

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QY 1 APPPLPDPKFEKSKAALLAARGPEELCTERLEDELVCFWMEAAAGVPGNYFSYOLE 60
DB 25 ASPSPLPDPKFEKSKAALLASRGSEELCTORLEDELVCFWMEAAASGM-DFNYFSYOLE 83
QY 61 DEPWKLCRLHQAPRTAGAVFWCSLPTADTSSFVPLELKVTAASGAPRYHRYIHNEVYL 120
DB 84 GESRKSRLHQAPRTAGAVFWCSLPTADTSSFVPLELKVTAASGAPRYHRYIHNEVYL 143
QY 121 LDAPVGLVARLADESGHVVLRWLPPEETPMTHIREVDVDSAGNAGSVQRYEILLEGRT 180
DB 144 LDAPVGLVARLADESGHVVLRWLPPEETPMTHIREVDVDSAGNAGSVQRYEILLEGRT 203
QY 181 CVLSNLRGRTYRTFAVRARMAEPSPFGFWSANSEPVSLITPSDLD 225
DB 204 CVLSNLRGRTYRTFAVRARMAEPSPFGFWSANSEPVSLITPSDLD 248

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373		

[illegible]

OY 126 GLVARL--ADESGHVLRLPPEPTMTSH--IRYEVDSVAGNGAGSVORVEILEGRT 179
 DB 132 NTLLEKHEDEKRPVLMKIMSPPTMDVKSQWETIIQYELRLKPKATMDETHPTLQ--T 189
 OY 180 ECVSLNLRGRTRYTAVRARMAPSGFWSAMSEPVSLTLPD 223
 DB 190 QKIFNLPGORYLVQIRCK---PDH-GYVSEWSPSSSIQIPND 229
 RESULT 7
 PRLR CEREL STANDARD: PRT: 581 AA.
 AC 028235;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE prolactin receptor precursor (PRL-R).
 GN PRLR.
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_Taxid=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96030711; PubMed=7561644;
 RA Clarke L.A., Edey M., London A.S., Randall V.A., Postel-Vinay M.C.,
 RA Kelly P.A., Jabbour H.N.;
 RT "Expression of the prolactin receptor gene during the breeding and
 RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
 RT expression of two forms in the testis.";
 RL J. Endocrinol. 146:313-321(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: X94953; CAA64419.1; -
 DR HSSP: P14787; IAN3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 24
 FT CHAIN 25 581
 FT DOMAIN 25 234
 FT TRASMEN 235 258
 FT DOMAIN 259 581
 FT DOMAIN 25 122
 FT DOMAIN 123 227
 FT DISULFD 75 46
 FT DISULFD 59 86
 FT CAROHD 132 132
 FT CAROHD 233 233
 FT CAROHD 233 233
 SEQUENCE 581 AA; 65159 MW; 975E47CB63CF28EC CRC64;
 Query Match 12.6%; Score 151; DB 1; Length 581;
 Best Local Similarity 23.9%; Pred. No. 1.3e-06;

Matches 51; Conservative 36; Mismatches 100; Indels 26; Gaps 9;
 OY 23 PERLCFTLRLEDLCFMEEAASAGVPCNYSFVLEDEPMKICLHOAPTARGAVRFW 82
 DB 31 PIKIKRSFGKELTFPCWMEPGSDGL-PNNYLLTYKBE-----TLIHCPDYKIGPRT 85
 OY 83 CSLIPADTSSFVPLELRVA-----ASGAPRYHRYHINEVLLDAPVGLVARL--AD 133
 DB 86 CYFSKHKTSIMKIYVITVAINQMVGSSSDPLY---VDVTYIEPEPPANLTLELKHPRD 142
 OY 134 ESGHVLRLPPEPTMTSH--IRYEVDSVAGNGAGSVORVEILEGRT 190
 DB 143 RRPVAVRARMAPSGFWSAMSEPVSLTLPD 223
 OY 191 RYTFVAVRARMAPSGFWSAMSEPVSLTLPD 223
 DB 201 KYLVYRCK---PDH-GYVSEWSPSSSIQIPND 229
 RESULT 8
 PRLR RABIT STANDARD: PRT: 616 AA.
 AC P14787;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE prolactin receptor precursor (PRL-R).
 GN PRLR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=89184578; PubMed=2928321;
 RA Edey M., Jolicoeur C., Levy-Meyruels C., Dusanter-Fourt I.,
 RA Petridou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;
 RT "Identification and sequence analysis of a second form of prolactin
 RT receptor by molecular cloning of complementary DNA from rabbit
 RT mammary gland.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
 RN [2]
 RP 3D-STRUCTURE MODELING OF 30-228.
 RX MEDLINE=97248733; PubMed=9094747;
 RA Halaby D., Thoreau E., Djiane J., Mornon J.P.;
 RT "Homology modeling of rabbit prolactin hormone complexed with its
 RT receptor.";
 RL Proteins 27:459-468(1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC -----
 DR EMBL: J04510; AAA31457.1; -
 DR PIR: A30304; A30304.
 DR PDB: 1AN3; 03-DEC-97.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.

RESULT	10			
ID	PRLR COLLI	STANDARD;	PRT;	830 AA.
AC	090374:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Prolactin receptor precursor (PRL-R).			
GN	PRLR.			
OS	Columba livia (Domestic pigeon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauiria; Aves; Neognathae; Columbiformes; Columbidae; Columba.			
OX	NCBI_TaxId=8932;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=CropSac;			
RC	MEDLINE=94283267; PubMed=7516866;			
RX	Chen X., Horseman N.D.;			
RA	"Cloning, expression, and mutational analysis of the pigeon prolactin			
RT	receptor.";			


```

OY 23 PELLCTFERLEDLYCFWEBAASAGVPGNYSFSYQLEDEPWKLCRLHQAPFARGAVRFW 82
D 31 PRINCGRSLEKETFCSCWKPQSDGL-PTNYTLFYSKSDSE-----KIYECDDYKISGNS 85
OY 83 CSLPFAOTSSFPVLELRYTAA-----SGAPRYHRYIHINEVLLDAPVGLVARLADSG 136
D 86 CFYFNHNTNSMTYNTYITATNEIGSNSSDPQY---VDVTSIVGPGSPVNLTLFTQRYAN 142
OY 137 HAVLL--RMLPPPTMTSHIREVDVSAAGNSQVOREILEGRTECVLSNLGRTRTF 194
D 143 IMYIMAKWSPLLDASSNHLYHYELRLKPEKEEMETVPVGVOYQCKINRLNAGMRVYV 202
OY 195 AVRAMAPESFGFWSASSEPVSILTPSD 224
D 203 QVRC-MLDP---GEMSEMSERRIISGCL 228

RESULT 12
PRLR_HUMAN
ID PRLR_HUMAN STANDARD; PRT; 622 AA.
AC p16471; Q9B8X7;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90114212; PubMed=2558309;
RA Boutin J.-M., Ebery M., Shitota M., Jolicoeur C., Lesueur L.,
RA Ali S., Gould D., Djiane J., Kelly P.A.;
RT "Identification of a cDNA encoding a long form of prolactin receptor
RT in human hepatoma and breast cancer cells.";
RL Mol. Endocrinol. 3:1455-1461(1989).
RN 12
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99182102; PubMed=10084611;
RA Hu Z.-Z., Zhuang L., Meng J., Leonidires M., Dufau M.L.;
RT "The human prolactin receptor gene structure and alternative promoter
RT utilization: the generic promoter hPRLI and a novel human promoter
RT hP(N).";
RL J. Clin. Endocrinol. Metab. 84:1153-1156(1999).
RN 13
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Breast carcinoma;
RA Kline J.B., Clevenger C.V.;
RT "Characterization of a novel and functional human prolactin receptor
RT isoform (delta-s1 PRLr) containing only one extracellular
RT fibronectin-like domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN 14
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
RX Somers W., Ullsch W., de Vos A.M., Kossiakoff A.A.;
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";
RL Nature 372:478-481(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PRLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Delta-S1;
CC are produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL; M31661; AAA60174.1; -.
DR EMBL; AF091870; AAD32032.1; -.
DR EMBL; AF091863; AAD32032.1; JOINED.
DR EMBL; AF091864; AAD32032.1; JOINED.
DR EMBL; AF091865; AAD32032.1; JOINED.
DR EMBL; AF091866; AAD32032.1; JOINED.
DR EMBL; AF091867; AAD32032.1; JOINED.
DR EMBL; AF091868; AAD32032.1; JOINED.
DR EMBL; AF091869; AAD32032.1; JOINED.
DR EMBL; AF349939; AAK32703.1; -.
DR PIR; A40144; A40144.
DR PDB; 1BP3; 23-SEP-98.
DR MIM; 176761; -.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; Hematopo_receptor_L.F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L.F1; 1.
DR KW Receptor; Transmembrane; Glycoprotein; signal; Repeat;
KV Alternative splicing; 3D-structure.
FT SIGNAL 1
FT CHAIN 25 622 PROLACTIN RECEPTOR.
FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 258 POTENTIAL.
FT DOMAIN 259 622 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 123 227 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.
FT DISULFD 36 46 BY SIMILARITY.
FT DISULFD 75 86
FT CARBOHD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 24 124 MISSING (IN ISOFORM 2).
SQ SEQUENCE 622 AA; 69505 MW; DB7FD0328608C787 CMC64;

Query Match 10.7%; Score 128; DB 1; Length 622;
Best Local Similarity 23.8%; Pred. No. 0.00021;
Matches 50; Conservative 33; Mismatches 107; Indels 20; Gaps 9;
OY 23 PELLCTFERLEDLYCFWEBAASAGVPGNYSFSYQLEDEPWKLCRLHQAPFARGAVRFW 82
D 31 PRINCGRSLEKETFCSCWKPQSDGL-PTNYSLTYHREG-----TLMHECPDYITGFPNS 85
OY 83 CSLPFAOTSSFPVLELRYTAA--GAPRYHRY-IHINEVLLDAPVGL---VARLADSG 136
D 86 CFYFNHNTNSMTYNTYIMVNATNMQSSFSDELIVYIVYVOPDPLAVEVKQPEDRRP 145
OY 137 HAVLLRMLPPPTMTS---HIREVDVSAAGNSQVOREILEGRTECVLSNLGRTRTF 193
D 146 YIMIKWSPTLLDKTGFTLLYELRLKPEKA--EMELHFAQGQTEKILSLHFGQYVL 203
OY 194 FAVRAMAPESFGFWSASSEPVSILTPSD 223
D 204 QVRC---PDH-GYWSAMSPATFIQIPSD 229

RESULT 13
IL9R_HUMAN
ID IL9R_HUMAN STANDARD; PRT; 522 AA.
AC Q01113; Q14634;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-9 receptor precursor (IL-9R).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92302307; PubMed=1376929;
RA Renaud J.C., Druze C., Kermouni A., Housiau F., Uytendhoe C.,
RT van Roost E., van Snick J.;
RT "Expression cloning of the murine and human interleukin 9 receptor
RL cDNAs.";
RN Proc. Natl. Acad. Sci. U.S.A. 89:5690-5694(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94250901; PubMed=8193355;
RA Chang M.S., Engel G., Benedict C., Basu R., McIninch J.;
RT "Isolation and characterization of the human interleukin-9 receptor
RL gene.";
RN Blood 83:3199-3205(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Melanoma; PubMed=8666384;
RA Kermouni A., van Roost E., Arden K.C., Vermeesch J.R., Weiss S.,
RT Godelaine D., Flint J., Lurquin C., Szikora J.P., Higgs D.R.,
RA Marynen P., Renaud J.C.;
RT "The IL-9 receptor gene (IL9R): genomic structure, chromosomal
RT localization in the pseudautosomal region of the long arm of the sex
RT chromosomes, and identification of IL9R pseudogenes at 9pter, 10pter,
RT 16pter, and 18pter.";
RN Genomics 29:371-382(1995).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-9.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND SECRETED.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; M84747; AAA58679.1; -.
DR EMBL; S71404; AAB30844.2; ALT_SEQ.
DR EMBL; S71420; AAD14081.1; -.
DR EMBL; L39064; AAC29513.1; -.
DR PIR; B45268; B45268.
DR MIM; 300007; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003531; Hematopo_receptor_S_FL.
DR PROSITE; PS01355; HEMATOPO_REC_S_FL; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 40
FT CHAIN 1 522
FT DOMAIN 41 270
FT TRANSMEM 291 291
FT DOMAIN 292 522
FT DOMAIN 150 244
FT DOMAIN 429 439
FT DOMAIN 440 443
FT CARBOHYD 117 117
FT CARBOHYD 156 156
FT CONFLICT 331 331
FT CONFLICT 439 439
FT SEQUENCE 522 AA; 57333 MW; ECBC5C6342DE2BB2 CAC64;

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Query Match      10.6%  Score 126;  DB 1;  Length 522;
Best Local Similarity 24.6%  Pred. No. 0.00027;
Matches 58;  Conservative 25;  Mismatches 93;  Indels 60;  Gaps 13;

OY 21 RGPBB-DLCTEREDLVCFWEAASAGVGCGNLSFSYQLEDEPPKLCRLHQAP----- 73
      *  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 47 QGPPSRPTCTLTNNLRIDCHW-SAPBLGQG-----SSWLLFTSQAQAGTAK 94

QY 74 -TAGAVALFMSLPTADSSFPVLE-LVY---AASG-----APRRHRIHNE 117

Db 95 CILGSE--CTVLPPEAVLVSPDNFTTTFHCHNGSREQVSLDPEYLPRH----- 144

QY 118 VLLDAPGLVALRADESGHVLRN-LPPETPMTHRYEVDVSAGNGA-GSVORVEL 175

Db 145 -VKLDPPEDLOSNTS--SGHCILTMSTISPALEPMITLLSYELAFKKQDEAMQAOHRI 201

QY 176 EGRTCVLSNLRGRTYTFAVRAR-----MAEFSFGGFWMSAMSEPVSLTP 221

Db 202 VGVATWLLEAFELDPGFIEHARLRVQMATLEDDVVEEERYTGQMSQPCVCFQAP 257

RESULT 14

PRLR_MOUSE STANDARD; PRT; 608 AA.

AC 008501:062099; P15213; P15212;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NM_008501:062099; P15213; P15212;
RP STRAIN=C3H: TISSUE=Mammary gland;
RX MEDLINE=94085788; PubMed=8262385;
RA Moore R.C., Oka T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
RT long-form prolactin receptor.";
RL Gene 134:263-265(1993).
RN [2]
RN NM_008501:062099; P15213; P15212;
RP STRAIN=SWISS WEBSTER; TISSUE=Liver;
RX MEDLINE=93307149; PubMed=8319571;
RA Clarke D.L., Linzer D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the
RT mouse ovary.";
RL Endocrinology 133:224-232(1993).
RN [3]
RN NM_008501:062099; P15213; P15212;
RP STRAIN=FROM N.A. (FORM PRL-R3).
RA Sasaki M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NM_008501:062099; P15213; P15212;
RP STRAIN=FROM N.A. (FORM PRL-R3)
RC STRAIN=BALB/C; TISSUE=Mammary gland;
RA Edery M., Pezet A., Nandi S., Kelly P.A.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RN NM_008501:062099; P15213; P15212;
RP STRAIN=FROM N.A. (FORM PRL-R2 AND PRL-R1).
RC STRAIN=SWISS WEBSTER; TISSUE=Liver;
RX MEDLINE=89261824; PubMed=2725331;
RA Davis J.A., Linzer D.I.H.;
RT "Expression of multiple forms of the prolactin receptor in mouse
RT liver.";
RL Mol. Endocrinol. 3:674-680(1989).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: PRL-R1, PRL-R2 AND PRL-R3 (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBROECTIN TYPE III-LIKE DOMAINS.
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CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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 CC -----
 DR EMBL: L13593; AAC37641.1; -
 DR EMBL: L14811; AAA02686.1; -
 DR EMBL: D10214; BAA01066.1; -
 DR EMBL: X73372; CAA51789.1; -
 DR EMBL: M22959; AAA39977.1; -
 DR EMBL: M22958; AAA39976.1; -
 DR PIR: J0671; J0671.
 DR HSSP: P14787; IAN3.
 DR MGD: MGI:97763; Pr1r.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; FN3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 608
 FT DOMAIN 20 229
 FT TRANSMEM 230 253
 FT DOMAIN 254 608
 FT DOMAIN 20 117
 FT DOMAIN 119 222
 FT DISULFD 31 41
 FT DISULFD 70 81
 FT CARBOHD 54 54
 FT CARBOHD 99 99
 FT CARBOHD 127 127
 FT VARSPLIC 281 292
 FT VARSPLIC 293 608
 FT VARSPLIC 281 303
 FT VARSPLIC 304 608
 FT CONFLICT 558 558
 FT SEQUENCE 608 AA; 68240 MW; B8CE202B2E9CF6C CRC64;
 Query Match 10.6%; Score 126; DB 1; Length 608;
 Best Local Similarity 22.3%; Pred. No. 0.00032;
 Matches 47; Conservative 38; Mismatches 104; Indels 22; Gaps 8;
 QY 23 PELLCTERLELDVCFWEAASAGVGENYSFQLEDEPMKLCRLHQAPTARGAVRFW 82
 DB 26 PEIHCRCSPDKETFTCMWPGSDGGL-PTNYSILTVSKEGEK---NTYCPDYKTSGPSNS 80
 QY 83 CSLPTADRSSEVPLELRVTA-----ASGAPRYHRIHINEVLLDAPGL---VARLAD 133
 DB 81 CFFSQYVSIMKIYITVATNEMGSSISDPL---VDVTYVLEPPPNLLLEVAKQLD 137
 QY 134 ESGHVVLRMLPPETPM-TSHIRYEDVASGNCAGSVQVEILEGTECVLSNLKGRTRY 192
 DB 138 KTYLWVKMLPPTITDVKGMFTMEYELRLKSEADENWHHTGTQTKVVDLYRGKX 197
 QY 193 TFAVRAKMAEFSFGFWKSWSEPVSLIPSD 223
 DB 198 LVOTRCK---PDH-GYWSRMGQEKSEIETPND 224
 RESULT 15
 GHR_MOUSE STANDARD; PRT; 650 AA.
 ID GHR_MOUSE
 AC P16882; P16590; Q9R264;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Growth hormone receptor precursor (Gh receptor) (Gh binding protein)
 DE (GHRP) (Serum binding protein).

GN GHR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=89295449; PubMed=2739661;
 RA Smith W.C., Kuniyoshi J., Talamantes F.;
 RT "Mouse serum growth hormone (Gh) binding protein has Gh receptor
 RT extracellular and substituted transmembrane domains.";
 RL J. Mol. Endocrinol. 3:984-990(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX STRAIN=Swiss Webster, and DBA/2J;
 RM MEDLINE=99367316; PubMed=10425445;
 RA Moffat J.G., Edens A., Talamantes F.;
 RT "Structure and expression of the mouse growth hormone receptor/growth
 RT hormone binding protein gene.";
 RL J. Mol. Endocrinol. 23:33-44(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX STRAIN=Swiss Webster, and DBA/2J;
 RM MEDLINE=95080157; PubMed=7988474;
 RA Edens A., Southard J.N., Talamantes F.;
 RT "Mouse growth hormone receptor/binding protein and growth hormone
 RT receptor transcripts are produced from a single gene by alternative
 RT splicing.";
 RL Endocrinology 135:2802-2805(1994).
 RN [4]
 RP SEQUENCE OF 156-650 FROM N.A. (ISOFORM 1).
 RX STRAIN=C57BL;
 RM MEDLINE=95201642; PubMed=7894338;
 RA Zhou Y., He L., Kopechick J.J.;
 RT "An exon encoding the mouse growth hormone binding protein (mGHRP)
 RT carboxy terminus is located between exon 7 and 8 of the mouse growth
 RT hormone receptor gene.";
 RL Receptor 4:223-227(1994).
 RN [5]
 RP REVISIONS.
 RX STRAIN=C57BL;
 RA Zhou Y., He L., Kopechick J.J.;
 RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 25-41.
 RX MEDLINE=88288223; PubMed=3398846;
 RA Smith W.C., Colosi P., Talamantes F.;
 RT "Isolation of two molecular weight variants of the mouse growth
 RT hormone receptor.";
 RL Mol. Endocrinol. 2:108-116(1988).
 CC -1- FUNCTION: Isoform 1 is a receptor for pituitary gland growth
 CC hormone. Isoform 2 is a serum growth hormone binding protein that
 CC may play an important role in regulating the effective serum
 CC concentration of gh.
 CC -1- SUBUNIT: Isoform 1 is a homodimer.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC secreted (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1/mmw GHR (shown here) and 2/LMW
 CC GHR; are produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M33324; AAA37690.1; ALT_SEQ.
 DR EMBL: M31680; AAA37689.1; ALT_SEQ.
 DR EMBL: AF120489; AAD32556.1; -.

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DR EMBL: AF120481. AAD32556.1; JOINED.
DR EMBL: AF120482. AAD32556.1; JOINED.
DR EMBL: AF120483. AAD32556.1; JOINED.
DR EMBL: AF120484. AAD32556.1; JOINED.
DR EMBL: AF120485. AAD32556.1; JOINED.
DR EMBL: AF120486. AAD32556.1; JOINED.
DR EMBL: AF120487. AAD32556.1; JOINED.
DR EMBL: AF120488. AAD32556.1; JOINED.
DR EMBL: AF120487. AAD32555.1; JOINED.
DR EMBL: AF120481. AAD32555.1; JOINED.
DR EMBL: AF120482. AAD32555.1; JOINED.
DR EMBL: AF120483. AAD32555.1; JOINED.
DR EMBL: AF120484. AAD32555.1; JOINED.
DR EMBL: AF120485. AAD32555.1; JOINED.
DR EMBL: AF120486. AAD32555.1; JOINED.
DR EMBL: U49266. AAK62802.1; JOINED.
DR EMBL: U49268. AAK62802.1; JOINED.
DR EMBL: U43933. AAK62802.1; JOINED.
DR HSSP: P10912.1; HMM.
DR MGD: MGI:95708; Ghr.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041.1; fn3.1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1.1.
DR Receptor: Transmembrane; Glycoprotein; Signal; Alternative splicing.
KW SIGNAL 1 24
FT CHAIN 25 650 GROWTH HORMONE RECEPTOR.
FT DOMAIN 25 273 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 274 297 POTENTIAL.
FT DOMAIN 298 650 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 260 FIBRONECTIN TYPE-III.
FT DISULFID 56 66 BY SIMILARITY.
FT DISULFID 109 120 BY SIMILARITY.
FT CARBOHYD 123 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 271 296 DIOFPWFLIIIGIFGVAWLVFVIR -> GTRKSNQHPHO
EIDNHLXHOLRIKH (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
FT VARSPLIC 297 650 T -> A (IN REF. 6).
FT CONFLICT 25 25 G -> A (IN REF. 3 AND 4).
FT CONFLICT 162 162 G -> G (IN REF. 2).
FT CONFLICT 325 325 R -> A (IN REF. 2).
FT CONFLICT 423 423
SQ SEQUENCE 650 AA: 72783 MW: 9565380CAFO8931 CRC64;

Query Match 10.3%; Score 123.5; DB 1; Length 650;
Best Local Similarity 22.6%; Pred. No. 0.0006;
Matches 52; Conservative 39; Mismatches 88; Indels 51; Gaps 10;

QY 23 PELLLEFTELEDLVCFWEERASAGV-GPGNYSFSQLED-----EPWKICR 68
DB 51 PRRTKCRSPLELEFFSCYEWEGNDPDKTPEGSIOLYTAKRRESQROAARIAHEWTQEWREC- 109
QY 69 LHOAPTARGAVRWCSLPTADTSSFVPLELRYTAASGAPRYHRVHIINEVYLLDAPVGLV 128
DB 110 ---PDYVSAKNSCYFNSYTSIMWIPYCICKL-TNGDLDLQCKFYVDEIVQPPPIGLN 164
QY 129 ARLADES-----GHVVLRMLPPETPMTSH---IREVDVSAGNGAGSVORVEILGR-- 178
DB 165 WTLINISLIGIRGDIQVSMQPPNADVLKGMILLEYE-----IQYKEVNSKWK 213
QY 179 -----TECVLSNLGRRTYRTFAVARARMAEPFGGFWMSAMSEPVSLTP 221
DB 214 VMGPILWLYTCVPYSLRDKHEHYVRSR--QRSFEKY-SESEVELRVIFP 260
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